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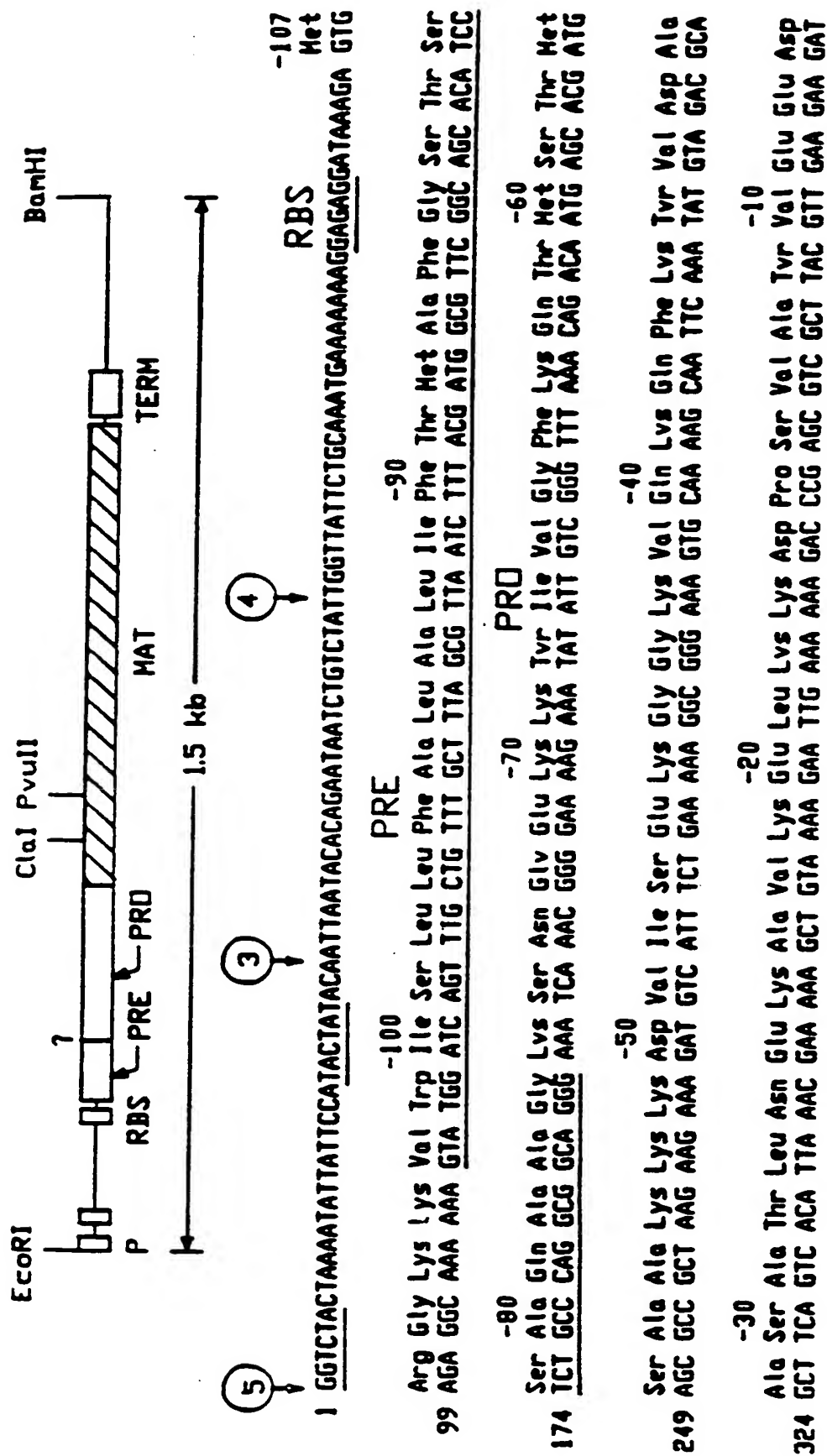


FIG.-1A

-1 | 1
MAT

His Bol Ala His Ala Tyr Ala Gln Ser Val Pro Tyr Gly Val Ser Gln Ile Lys Ala Pro Ala Leu His Ser Gln
399 CAC GTA GCA CAT GCG TAC GCG CAG TCC GTG CCT TAC GGC GTA TCA CAA ATT AAA GCC CCT GCT CTG CAC TCT CAA

20 30 40
Gly Tyr Thr Gly Ser Asn Val Lys Val Ala Val Ile Asp Ser Gly Ile Asp Ser Ser His Pro Asn Leu Lys Val
474 GGC TAC ACT GGA TCA AAT GTT AAT AAA GTA GCG GTT ATC GAC AGC GGT ATC GAT TCT TCT CAT CCT GAT TTA AAG GTA

50 60
Ala Gly Gly Ala Ser Met Val Pro Ser Glu Thr Asn Pro Phe Gln Asp Asn Asn Ser His Gly Thr His Val Ala
549 GCA AGC GGA GCC AGC ATG GTT CCT TCT TCT GAA ACA AAT CCT TTC CAA GAC AAC AAC TCT CAC GGA ACT CAC GTT GCC

70 80 90
Gly Thr Val Ala Ala Leu Asn Asn Ser Ile Gly Val Leu Gly Val Ala Pro Ser Ala Ser Leu Tyr Ala Val Lys
624 GGC ACA GTT GCG GCT CTT AAT AAC TCA ATC ATC GGT GTA TTA GGC GTT GCG CCA AGC GCA TCA CTT TAC GCT GTA AAA

100 110
Val Leu Gly Ala Asp Gly Ser Gly Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu Trp Ala Ile Ala Asn Asn Met
699 GTT CTC GGT GCT GAC GGT TCC GGC CAA TAC AGC TGG ATC ATT AAC GGA ATC GAG TGG GCG ATC GCA AAC AAT ATG

120 130 140
Asp Val Ile Asn Met Ser Leu Gly Gly Pro Ser Gly Ser Ala Ala Leu Lys Ala Ala Val Asp Lys Ala Val Ala
774 GAC GTT ATT AAC ATG AGC CTC GGC GGA CCT TCT GGT TCT GCT GCT TTA AAA GCG GCA GTT GAT AAA GCC GTT GCA

150
Ser Gly Val Val Val Val Ala Ala Ala Gly Asn Glu Gly Thr Ser Gly Ser Ser Thr Val Gly Tyr Pro Gly
849 TCC GGC GTC GTA GTC GTT GCG GCA GCC GGT AAC GAA GGC ACT TCC GGC AGC TCA AGC ACA GTG GGC TAC CCT GGT

FIG-1B

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170      Lvs Tyr Pro Ser Val Ile Ala Val Gly Ala Val Asp Ser Ser Asn Gln Arg Ala Ser Phe Ser Ser Val Gly Pro
924 AAA TAC CCT TCT GTC ATT GCA GTA GGC GCT GTT GAC AGC AGC AAC CAA AGA GCA TCT TTC TCA AGC GTA GGA CCT

      180
200      Glu Leu Asp Val Met Ala Pro Gly Val Ser Ile Gln Ser Thr Leu Pro Gly Asn Lvs Tyr Gly Ala Tyr Asn Gly
999 GAG CTT GAT GTC ATG GCA CCT GGC GTA TCT ATC CAA AGC AGC CTT CCT GGA AAC AAA TAC GGG GCG TAC AAC GGT

      210
220      Thr Ser Met Ala Ser Pro Pro His Val Ala Gly Asl Ala Ala Leu Ile Leu Ser Lys His Pro Asn Trp Thr Asn Thr
1074 ACG TCA ATG GCA TCT CCG CAC GCT GGC GGA GCG GCT GCT TTG ATT CTT TCT AAG CAC CCG AAC TGG ACA AAC ACT

      230
250      Gln Val Aro Ser Ser Leu Glu Asn Thr Thr Thr Lys Leu Gly Asp Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn
1149 CAA GTC CGC AGC AGT TTA GAA AAC ACC ACT ACA AAA CTT GGT GAT TCT TTG TAC TAT GGA AAA GGG CTG ATC AAC

      260
270      Val Gln Ala Ala Ala Gln DC
1224 GTA CAA GCG GCA GCT CAG TAA  AACATAAAACCGGCCCTTGGCCCGGGTTCCTTATTTTCTTCCTCGCATGTTCAAATCGGCTCC

      275
1316 ATATCGACGGATGGCTCCCTCTGAAATTTTAAAGAGAAACGGGGGTGACCCGGCTCAGTCCCGTAACGGGCAACTCCTGAACGCTCAATCGGCG

1416 CTTCCTGGTTCCGGTCAGCTCAATGCCATAACGGTGGGGGGTTCCTGATACCGGGAGACGGCATTCGTAATCGGATC

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FIG.-1C

1	A	Q	S	V	P	.	G	A	P	A	.	H	.	.	G	20	
21	.	T	G	S	.	V	K	V	A	V	.	D	.	G	H	P	40
41	D	L	.	.	.	G	G	A	S	.	V	P	Q	D	60
61	.	N	.	H	G	T	H	V	A	G	T	.	A	A	L	N	N	S	I	G	80
81	V	L	G	V	A	P	S	A	.	L	Y	A	V	K	V	L	G	A	.	G	100
101	S	G	.	.	S	.	L	.	.	G	.	E	W	A	.	N	120
121	V	.	N	.	S	L	G	.	P	S	.	S	A	.	.	140
141	G	V	.	V	V	A	A	.	G	N	.	G	160
161	Y	P	.	.	Y	A	V	G	A	.	.	180
181	D	.	.	N	.	.	A	S	F	S	.	.	G	.	.	L	D	.	.	A	200
201	P	G	V	.	.	Q	S	T	.	P	G	.	.	Y	.	.	.	N	G	T	220
221	S	M	A	.	P	H	V	A	G	A	A	A	L	.	.	.	K	.	.	.	240
241	W	.	.	.	Q	.	R	.	.	L	.	N	T	.	.	.	L	G	.	.	260
261	.	.	Y	G	.	G	L	.	N	.	.	A	A	270

FIG. 2

Comparison of subtilisin sequences from:

B. amyloliquefaciens
B. subtilis
B. licheniformis
B. lentus

01	10	20	30	
A Q S V P Y G V S Q I K A P A L H S Q G Y T G S N V K V A V I D S G I D S S H P				
A Q S V P Y G I S Q I K A P A L H S Q G Y T G S N V K V A V I D S G I D S S H P				
A Q T V P Y G I P L I K A D K V Q A Q G F K G A N V K V A V L D T G I Q A S H P				
A Q S V P W G I S R V Q A P A A H N R G L T G S G V K V A V L D T G I S T A H P				
41	50	60	70	
D L K V A G G A S H V P S E T N P F Q D N N S H G T H V A G T V A A L N N S I G				
D L N V R G G A S F V P S E T N P Y Q D G S S H G T H V A G T I A A L N N S I G				
D L N V V G G A S F V A G E A Y N A T D G N G H G T H V A G T V A A L D N T T G				
D L N I R G G A S F V P G E A P S T Q D G N G H G T H V A G T I A A L N N S I G				
81	90	100	110	
V L G V A P S A S L Y A V K V L G A D G S G Q Y S W I I N G I E W A I A N N M D				
V L G V S P S A S L Y A V K V L D S T G S G Q Y S W I I N G I E W A I S N N M D				
V L G V A P S V S L Y A V K V L N S S G S G S Y S G I V S G I E W A T N G M D				
V L G V A P S A E L Y A V K V L G A S G S G S V S S I A Q G L E W A G N G M H				
121	130	140	150	
V I N M S L G G P S S G S A A L K A A V D K A V A S G V V V A A A A G N E G T S G				
V I N M S L G G P T G S T A L K T V V D K A V S S G I V V A A A A G N E G S S G				
V I N M S L G G A S G S T A M K Q A V D N A Y A R G V V V A A A A G N S G N S G				
V A N L S L G S P S P S A T L E Q A V N S A T S R G V L V A A A S G N S G A G S				

FIG 3/A

161 S S S T V G Y P G K Y P S S V I A V G A V D S S N Q R A S F S S V G P E L D V M A
S S T V G Y P P A K Y P S S T I A V G A V N S S N Q R A S F S S A G S E L D V M A
S T N T I G Y P A K Y D S S V I A V G A V D S S N Q R A S F S S V G A E L E V M A
* * * I S Y P A R Y A N A H A V G A T D Q N N R A S F S S Q Y G A G L D I V A
170
180
190
201 P G V S I Q S T L P G C N K Y G A Y N G T S M A S P H V A G A A A L I L S K H P N
P G V S I Q S T L P G C T Y G A Y N G T S M A S P H V A G A A A L I L S K H P T
P G A G V Y S T Y P C S T Y A S L N G T S M A S P H V A G A A A L I L S K H P N
P G V N V Q S T Y P C S T Y A S L N G T S M A S P H V A G A A A L V K Q K N P S
210
220
230
241 W T N T Q V R S S L E N T T T K L G D S F Y Y G K G L I N V Q A A A Q
W T N A Q V R R L E S T A T T Y L G N S F Y Y G K G L I N V Q A A A Q
L S A S Q V R R L S S T A T T Y L G S S F Y Y G K G L I N V E A A A Q
W S N V Q I R N H L K N T A T S L G S T N L Y C S G L V N A E A A T R
250
260
270

FIG 3/B

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